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REMARKS

Claims 1-27 are pending in the instant application. Applicants have amended claims 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 19, 20, 23, 24, 26, and 27 to more fully conform with U.S. practice and to delete multiple dependencies. A copy of the marked up claims showing the amendments, as well as a clean copy of the claims encompassing the amendments, is attached hereto.

Applicants respectfully assert that all amendments are fairly based on the specification, and respectfully request their entry.

Applicants believe that the claims, as amended, are in allowable form, and earnestly solicit the allowance of claims 1-27.

Respectfully submitted,



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Amended Claims (marked up copy showing amendment(s))

[CLAIMS]

WHAT IS CLAIMED IS:

1. (amended) A set of libraries of genes which code for proteins which are capable of specific binding interactions with a specific binding partner by amino acid residues at at least two specified positions including a first specified position and at least one other specified position, which set of libraries [consists of]comprises:

a) 6 to 20 libraries in which each library has a triplet that codes for at least one but less than 20 amino acids at said first specified position, and is [randomised]randomized at the or each triplet coding for the said at least one other specified position, the arrangement being such that interactions of the proteins coded for by the said 6 to 20 libraries with a specific binding partner identifies a triplet that codes for an amino acid at the said first specified position that takes part in the specific binding interaction, and

b) 6 to 20 libraries in each of which libraries said first specified position is [randomised]randomized and a different one of said at least one other specified positions has a triplet that codes for at least one but less than 20 amino acids.

2. (amended) The set of libraries of genes as claimed in claim 1, which set of libraries [consists of]comprises:

a) 12 libraries in which each library has a triplet that codes for one or several but less than 20 amino acids at the said first determined position, the triplets being as shown in Table 1 or Table 2, and

b) 12 libraries of corresponding design for each of the said one or more other determined positions.

3. (amended) The set of libraries of genes as claimed in claim 1[or claim 2], wherein the genes code for zinc fingers.

4. (amended) The set of libraries of genes as claimed in claim 3, which set [consists of]comprises 36 libraries in three groups of 12 libraries which code for amino acids at the -1 and +3 and +6 positions respectively.

5. (amended) The set of libraries of genes as claimed in claim 3[or claim 4], wherein each gene codes for a protein comprising [3]three zinc fingers.

6. (amended) The set of libraries of genes as claimed in claim 5, wherein each gene codes for a protein having the sequence (SEQ ID NO: 2)

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

where X is any amino acid.

7. (amended) A set of libraries of proteins, which proteins are capable of specific binding interactions with a specified binding partner by amino acid residues at at least one specified position including a first specified position and at least one other specified position, which set of libraries [consists of]comprises:

a) 6 to 20 libraries in which each library has at least one but less than 20 amino acid residues at the said first specified position and is [randomised]randomized at the said at least one other determined position, the arrangement being such that interaction of the 6 to 20 libraries with a specific binding partner identifies an amino acid residue at the said first specified position that takes part in the specific binding interaction, and

b) 6 to 20 libraries in each of which libraries said first specified position is [randomised]randomized and a different amino acid is present at at least one other specified position.

8. (amended) The set of libraries of proteins as claimed in claim 7, which set of libraries [consists of]comprises:

a) 20 libraries in which each library has one specified amino acid residue at the said first determined position and is [randomised]randomized at the said one or more other determined positions, and

b) 20 libraries of corresponding design for each of the said one or more other determined positions.

9. (amended) The set of libraries or proteins as claimed in claim 7[or claim 8], wherein the proteins are zinc fingers.

10. (amended) The set of libraries of proteins as claimed in claim 7, which set [consists of]comprises 60 libraries in three groups of 20 libraries with specified amino acids at the -1 and +3 and +6 positions respectively.

11. (amended) The set of libraries of proteins as claimed in claim 9[or claim 10], wherein each protein comprises three zinc fingers.

12. (amended) The set of libraries of proteins as claimed in claim 11, wherein each protein has the sequence (SEQ ID NO: 2)

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

T G E K P Y K C P E C G K S F S X K S X L V X H Q R T H

where X is any amino acid.

13. (amended) A set of libraries of genes which code for the set of libraries of proteins defined in [any one of claims 7 to 12]claim 7.

14. (amended) A method of identifying a protein which interacts with a specific binding partner, which method comprises providing a set of libraries of proteins as defined in [any one of claims 7 to 12]claim 7, incubating the specific binding partner with each library of the set, observing

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specific binding interactions with certain libraries of the set, and using the observations to identify a protein which interacts with the specific binding partner.

19. (amended) The method as claimed in claim 18, wherein the sets of libraries of proteins are [immobilised]immobilized on scintillation proximity assay surfaces and the specific binding partner is radiolabelled.

20. (amended) The method of claim 18[or claim 19], wherein after incubation the scintillation proximity assay surfaces are washed to distinguish stronger specific binding interactions from weaker ones.

23. (amended) The method as claimed in claim 21,[or claim 22] wherein after incubation the binding interactions are washed to distinguish stronger specific binding interactions from weaker ones.

24. (amended) A protein having the sequence (SEQ ID NO: 1)

T G E K P Y K C P E C G K S F S [.]K K S [+]H L V [\$]A H Q R T H
T G E K P Y K C P E C G K S F S [.]K K S [+]H L V [\$]A H Q R T H
T G E K P Y K C P E C G K S F S [.]K K S [+]H L V [\$]A H Q R T H.

26. (amended) A method of constructing [randomised]randomized gene libraries in which the number of genes is the same as the number of encoded proteins and which contain no termination codons at the predetermined positions of [randomisation]randomization, the method comprising the steps of:

a) providing a template oligonucleotide which is fully [randomised]randomized at predetermined codon positions;

b) for each predetermined codon position providing a pool of selection oligonucleotides, wherein each member of said pool contains a different codon selected from the group [consisting of]comprising:

AAA, AAC, ACC, AGC, ATG, ATT, CAG, CAT, CCG, CGC, CTG, GAA,

GAT, GCG, GGC, GTG, TAT, TGG, TGC, TTT.

at the predetermined codon position;

- c) selecting one or more selection oligonucleotides from each pool in order to encode the required gene or library;
- d) allowing the ligated selected oligonucleotides from each pool to [hybridise]hybridize with the template oligonucleotide;
- e) forming one or more constructs by ligating the [hybridised]hybridized selection oligonucleotides together;
- f) removing a region from a gene of interest corresponding to the [hybridised]hybridized product from step e);
- g) forming a gene library or genes by ligating the products from step e) into the said gene of interest wherein the said gene of interest is contained within a suitable expression vector.

27. (amended) A method of producing proteins encoded by the [randomised]randomized gene libraries of claim 26 comprising the steps of:

- a) transforming a suitable host cell with the gene or gene library of claim [27]26 construct;
- b) expressing the genes to form proteins;
- c) purifying the proteins.

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